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## Meningococcal carriage among a university student population – United States, 2015

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### Abstract

**Objectives**—Several outbreaks of serogroup B meningococcal disease have occurred among university students in recent years. In the setting of high coverage of the quadrivalent meningococcal conjugate vaccine and prior to widespread use of serogroup B meningococcal vaccines among adolescents, we conducted surveys to characterize the prevalence and molecular characteristics of meningococcal carriage among university students.

**Methods**—Two cross-sectional oropharyngeal carriage surveys were conducted among undergraduates at a Rhode Island university. Isolates were characterized using slide agglutination, real-time polymerase chain reaction (rt-PCR), and whole genome sequencing. Adjusted prevalence ratios and 95% confidence intervals were calculated using Poisson regression to determine risk factors for carriage.

**Results**—A total of 1837 oropharyngeal specimens were obtained from 1478 unique participants. Overall carriage prevalence was 12.7–14.6% during the two survey rounds, with 1.8–2.6% for capsular genotype B, 0.9–1.0% for capsular genotypes C, W, or Y, and 9.9–10.8% for nongroupable strains by rt-PCR. Meningococcal carriage was associated with being male,

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#### Conflict of interest statement

We declare that we have no conflicts of interest.

#### Meetings

This work has not been previously presented at any meetings or scientific conferences.

#### Disclaimer

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

smoking, party or club attendance, recent antibiotic use (inverse correlation), and recent respiratory infections.

**Conclusions**—In this university setting, the majority of meningococcal carriage was due to nongroupable strains, followed by serogroup B. Further evaluation is needed to understand the dynamics of serogroup B carriage and disease among university students.

### Keywords

Meningococcal disease; Carriage; Meningococcal vaccines; *Neisseria meningitidis*; Meningococcal infections

## 1. Background

Meningococcal disease is a rare but serious illness resulting in high rates of morbidity and mortality. Transmission of the causative organism, *Neisseria meningitidis*, occurs through close contact with respiratory secretions, resulting primarily in asymptomatic nasopharyngeal carriage and rarely, invasive meningococcal disease. Adolescents and young adults in the United States are at increased risk of meningococcal carriage and disease due to increased social mixing, crowded living conditions, smoking, and other behaviors [1–4].

The Advisory Committee on Immunization Practices (ACIP) recommends routine vaccination of adolescents with a quadrivalent meningococcal conjugate vaccine (MenACWY) at age 11 or 12 years, with a booster dose at age 16 years to sustain protection through early adulthood [5]. Like other conjugate vaccines, MenACWY (MenACWY-D [Menactra®, Sanofi Pasteur [6]], MenACWY-CRM [Menveo®, Novartis [7]]) may reduce acquisition of nasopharyngeal carriage, and thus transmission, when high coverage is achieved, though data are limited [8–10]. Since implementation of the adolescent MenACWY program in 2005, coverage with at least one dose of MenACWY among 13–17 year olds reached 81.3% in 2015 [11]. Incidence of serogroup C and Y meningococcal disease among adolescents has subsequently declined, with serogroup B *Neisseria meningitidis* becoming the leading cause of meningococcal disease in this age group [12].

In 2014 and 2015, two serogroup B meningococcal (MenB) vaccines, MenB-4C (Bexsero®, GlaxoSmithKline) and MenB-FHbp (Trumenba®, Pfizer), were licensed for use in the United States [13,14]. In 2015, ACIP recommended that adolescents and young adults aged 16–23 years may be vaccinated with a MenB vaccine based on individual clinical discretion [15]. MenB vaccines are routinely recommended for certain persons aged ≥10 years at increased risk of serogroup B meningococcal disease, including during an outbreak of serogroup B meningococcal disease [16]. The impact of MenB vaccines on carriage remains under investigation [8,17,18].

In the context of high adolescent MenACWY coverage and low meningococcal disease incidence, with a predominance of outbreaks and sporadic disease now due to serogroup B, there is little recent data on the prevalence and serogroup distribution of carried *N. meningitidis* among U.S. university students. We conducted a carriage evaluation among undergraduate students at a Rhode Island university in a non-outbreak setting prior to

widespread availability of MenB vaccines to determine prevalence and molecular characteristics of meningococcal carriage and identify risk factors for carriage in this population.

## 2. Materials and methods

### 2.1. Study design

Two cross-sectional oropharyngeal carriage surveys were conducted in March (round 1) and April (round 2) 2015 at a Rhode Island university ('University A'), with participants recruited by convenience sampling among an undergraduate student population of 6320. All undergraduate students aged 18 years or older were eligible for voluntary participation and were recruited through emails and printed materials. University A is in the same city as Providence college, which experienced an outbreak of serogroup B meningococcal disease, with two cases reported among an undergraduate population of 4500 students, in February 2015 [19]. Though not assessed formally, university officials speculate there is minimal interaction between students at the two universities, and no cases of meningococcal disease were reported at University A.

### 2.2. Data and specimen collection

Enrollment and specimen collection were performed in common areas of the university, such as the student center and adjacent to a large cafeteria. Upon enrollment, all participants provided written informed consent and completed a self-administered questionnaire consisting of demographic information and potential factors associated with meningococcal carriage, including university year, living arrangements, history of tobacco and marijuana use, attendance at parties and bars, upper respiratory infection in the past 14 days, and history of antibiotic use in the past 30 days. MenACWY and MenB vaccination status was obtained through abstraction of student medical records at the university health center, where vaccination records are submitted upon university matriculation and maintained thereafter. As no MenB vaccine doses were documented in participant medical records and the carriage evaluation took place within five months of U.S. licensure of the first MenB vaccine and prior to ACIP recommendations for use of MenB vaccines among healthy adolescents and young adults, we assumed all participants to be unvaccinated with MenB.

Oropharyngeal swabs from each tonsillar pillar and the posterior pharynx were collected by trained personnel using bifurcated swabs. One swab was directly inoculated onto Modified Thayer–Martin (MTM) media (BD BBL, Sparks, MD) for culture. Inoculated media were stored in CO<sub>2</sub>-enriched Mitsubishi boxes at room temperature along with a positive control plate inoculated with *N. lactamica*. Inoculated plates and specimens were transported to the Rhode Island State Health Department Laboratory for primary testing with a maximum delay of four hours.

### 2.3. Laboratory methods

Inoculated culture plates were streaked, incubated at 37 °C (5% CO<sub>2</sub>), and examined for bacterial growth after 24, 48, and 72 h. Colonies with typical Neisserial morphology underwent Gram staining and were sub-cultured onto blood and/or chocolate agar plates. A

single colony per participant per round was selected for further characterization. At a species level, *N. meningitidis* was identified using Gram stain, oxidase test (Hardy Diagnostics; Santa Maria, CA), API NH strip (bioMérieux; Durham, NC), and *sodC* PCR assay [20,21]. Once confirmed as *N. meningitidis*, serogroup was determined by slide agglutination and capsular genotype by real-time PCR (rt-PCR). Expression of the capsular polysaccharide was determined by slide agglutination for serogroups A, B, C, E, W, X, Y, and Z (BD DIFCO; Franklin Lakes, NJ; and Thermo Scientific Remel; Waltham, MA). rt-PCR was used to detect the capsule biosynthesis genes specific for serogroups A, B, C, W, X, and Y [22]. An isolate was defined as nongroupable by slide agglutination when it autoagglutinated or did not agglutinate. As previously described, carriage isolates are commonly nongroupable phenotypically due to a low level or absence of capsule gene expression, while these isolates may still contain the capsule biosynthesis genes as detected by rt-PCR [23,24]; because of this, nongroupable genotype was independently defined by rt-PCR as no amplification in any serogroup-specific PCR assay.

For further characterization of serogroup B isolates and other isolates with discrepant results (e.g., discrepant NH strip and *sodC* results), genomic DNA was prepared for whole genome sequencing (WGS) on Illumina MiSeq platform (250 × 250 cycle paired-end sequencing kit; San Diego, CA) using 5 Prime ArchivePure DNA Purification kit (Gaithersburg, MD), Ampure (Beckman Coulter Inc.; Indianapolis, IN), and dual-index NEBNext Ultra sequencing libraries (New England Biolabs Inc.; Ipswich, MA). Published primer sequences were used to extract the seven meningococcal MLST house-keeping genes, *fetA*, and *porA* from CLC (v8.5.1; Qiagen; Waltham, MA) assembled WGS data [25]. After running extracted sequences through BLAST against the *Neisseria* PubMLST database, MLST sequencing type (ST) and clonal complex (CC), outer membrane (FetA and PorA) types and vaccine antigens (FHbp, NhbA, and NadA) were determined [26,27]. As previously described, a combination of the three nomenclature systems was used for FHbp type (Oxford numeric identifier followed by Pfizer subfamily and Novartis variant) [28].

## 2.4. Data analysis

Descriptive analyses were conducted for demographic and risk factor information. Significant differences ( $P < .05$ ) by round were assessed using a chi-square test for categorical variables and the Wilcoxon-Mann-Whitney test for continuous variables. The prevalence of meningococcal carriage overall and by serogroup and capsular genotype was determined for each survey round. To determine factors associated with overall carriage, prevalence ratios were calculated with bivariate Poisson regression analyses using generalized estimating equations and an exchangeable correlation structure to account for correlation of observations from individual participants across rounds. Collinearity and interactions were assessed, given the potential relatedness of several variables (e.g., smoking and partying, upper respiratory tract infection and use of antibiotics). Factors found to be significantly associated with carriage at  $P < .1$  were included in a multivariable model. Factors that remained significant at  $P < .05$  were considered to be independent predictors of meningococcal carriage. All data analyses were conducted using SAS 9.3 (SAS Institute, Cary, North Carolina).

## 2.5. Ethical review

This investigation was determined to be a public health evaluation and designated as non-research by the Centers for Disease Control and Prevention Human Research Protection Office, the chair of the Rhode Island Department of Health Institutional Review Board (IRB), and the chair of University A IRB, and therefore did not require full IRB review. Participation was voluntary and written informed consent was obtained from all participants by trained survey staff. Participants received a \$5 retail gift card for completion of the survey.

## 3. Results

In total, 1845 participants were enrolled in two carriage evaluation rounds. Among these, 8 were excluded due to a missing questionnaire or specimen, or duplicate specimen submission. Thus, 1837 oropharyngeal specimens, including 1076 (58.6%) specimens in round one and 761 (41.4%) in round two, were collected from 1478 unique participants. Three hundred fifty-nine participants were enrolled in both rounds. Characteristics of participants are shown in Table 1.

Among 1837 oropharyngeal specimens collected, 248 meningococcal isolates were recovered during the two survey rounds, including 137 of 1076 (12.7%) specimens in round one and 111 of 761 (14.6%) specimens in round two (Table 2). By slide agglutination, 0.7% of participants in each round carried meningococci that expressed the serogroup B capsule. By rt-PCR, 1.8% and 2.6% of participants carried capsular genotype B *N. meningitidis* in rounds one and two, respectively. Total carriage of *N. meningitidis* serogroups or capsular genotypes C, W, or Y ranged from 0.0 to 0.2% by slide agglutination and 0.9–1.0% by rt-PCR in the two rounds. Among participants carrying *N. meningitidis*, the majority carried nongroupable strains: 11.6–13.8% by slide agglutination and 9.9–10.8% by rt-PCR.

Of the 359 participants that took part in both carriage survey rounds, 45 participants (12.5%) were identified as carriers during at least one of the rounds and 29 (8.1%) were carriers in both rounds. From round one, 33 participants (9.2%) were identified as carriers; all isolates from these participants were nongroupable by slide agglutination, and the majority were also nongroupable by rt-PCR ( $n = 27$ , 81.8%), with 6 capsular genotype B isolates identified. In round two, a total of 42 (11.4%) participants were found to be carriers, including 29 carriers from round one that remained carriers in round two: 28 (96.6%) remained nongroupable by slide agglutination and one (3.4%) participant was found to carry serogroup B. The majority of nongroupable isolates by slide agglutination ( $n = 35$ , 83.3%) were also predominantly nongroupable by rt-PCR, with seven (16.7%) capsular genotype B isolates identified. Twelve additional new carriers were identified in round two and all acquired nongroupable *N. meningitidis* by slide agglutination. Of these isolates, six (50%) were capsular genotype B by rt-PCR and six (50%) were also nongroupable by rt-PCR.

Among 39 isolates identified as capsular genotype B by rt-PCR, 23 sequence types (ST) belonging to 9 clonal complexes (CC) were identified, including one new ST (12750). (Table 3). The most common CCs detected were CC41/44 Lineage 3 ( $n = 8$ ), CC32/ET-5 ( $n = 10$ ) and CC35 ( $n = 9$ ). ST-9069, the strain associated with the outbreak at Providence

College, was not identified among meningococcal carriers at University A. Further characterization of capsular genotype B isolates for PorA, FetA, FHbp, and NhbA are described in Table 3.

In bivariate Poisson regression analysis, an increased risk of carriage due to any serogroup or capsular genotype was associated with participation in round two of the evaluation; being male; going out to bars/parties at least one time per week on average; smoking tobacco or marijuana in the past 30 days; being exposed to second hand smoke in the last 30 days; and having had an upper respiratory tract infection in the last 14 days (Table 4). Residing in a residence hall and antibiotic use in the last 30 days were associated with reduced risk of carriage. Age, university class year, and MenACWY vaccine receipt were not associated with carriage. Collinearity and interactions were assessed but no significant associations were found.

In a multivariable analysis, participation in round two (aPR 1.20 [95% CI 1.01–1.42]), male sex (aPR 1.66 [95% CI: 1.29–2.14]), going out to bars/parties at least one time per week on average (aPR 2.03 [95% CI: 1.52–2.72]), tobacco use in the past 30 days (aPR 1.53 [95% CI: 1.21–1.94]), and an upper respiratory tract infection in the past 14 days (aPR 1.23 [95% CI: 1.001–1.51]) remained independently associated with carriage. Antibiotic use in the last 30 days continued to be inversely associated with carriage (aPR 0.42 [95% CI: 0.27–0.65]) (Table 4).

## 4. Discussion

Although rates of meningococcal disease in the United States are currently at historic lows, cases and outbreaks of meningococcal disease continue to occur among university students [29]. In our evaluation at a university with high MenACWY vaccine coverage, prior to widespread MenB vaccine availability, we found that prevalence of *N. meningitidis* carriage was 12.7–14.6%. This prevalence is higher than the 3.2–8% reported in recent carriage evaluations among U.S. high school and university-aged persons [3,30,31]. The low prevalence of encapsulated isolates, with few serogroup B and a near-absence of serogroups C and Y *N. meningitidis*, is consistent with the epidemiology of invasive meningococcal disease in this age group, which is characterized by overall low disease incidence, a predominance of cases due to serogroup B, and declines in the proportion of cases due to serogroups C and Y [32].

This evaluation, performed in a university population without recent meningococcal disease cases, provides an opportunity to compare characteristics of meningococcal carriage with those described at two other universities (neighboring Providence College, and a large, public university in Oregon) that experienced serogroup B meningococcal disease outbreaks and implemented three-dose MenB-FHbp vaccination campaigns during similar time periods in 2015–2016. Overall carriage and serogroup B-specific *N. meningitidis* carriage prevalence in the University A population was roughly half of that observed at Providence College, where overall carriage rates were 20–24% and capsular genotype B carriage was 4% by rt-PCR. Carriage in University A students was similar to the 11–17% overall carriage and 1–2% capsular genotype B-specific carriage observed at the university in Oregon



[17,18]. While these three universities differ in terms of size, university type (public or private), region of the country, epidemiologic situation, and MenB vaccination status, carriage in all three was characterized by a predominance of nongroupable meningococcal isolates and relatively low prevalence of capsular genotype B meningococcal carriage. Similar to these other two universities, and consistent with previous reports in the literature, meningococcal carriage at University A was associated with being male, smoking, attending parties, bars, or clubs, using antibiotic recently (inverse correlation), and having a recent upper respiratory tract infection [33–37].

Prevalence of capsular genotype B meningococcal carriage remained stable across the two survey rounds in our evaluation, and the strain causing the outbreak at Providence College (ST-9069) was not recovered from our university population. The few capsular genotype B isolates that were recovered in our evaluation displayed high genetic diversity. Of the clonal complexes identified among the capsular genotype B isolates, CC32/ET-5, CC35, and CC41/44 lineage 3 were the most common. These hyper-invasive lineages, found globally from carriage and invasive isolates, were previously associated with university outbreaks in California, New Jersey, and Oregon [24]. These hyper-invasive lineages, along with other identified clonal complexes (CC162, CC213, CC865, CC4821), have also been reported in the United States and Europe as carriage isolates in previous evaluations [3,23,30,38,39].

The detected vaccine antigen types (FHbp, NhbA, and NadA) in our evaluation were also observed among sporadic and carriage isolates globally and in the United States. [23,28,40]. Among serogroup B isolates, we found that FHbp variant A/v2–3 predominated, NadA was unrepresented, and all isolates had an NhbA antigen type. Seventeen percent of serogroup B carriage isolates possessed one or more specific MenB vaccine subvariants (2 isolates with FHbp subvariant 1/NadA-1.1, 4 with NhbA subvariant p0002, and 1 with FHbp subvariant 45) included in either the MenB-4C or the MenB-FHbp vaccine. The remaining 83% of serogroup B isolates, with subvariants not included in the vaccines, may still be covered by the vaccines through cross-reactivity [41]. However, implications of this potential vaccine coverage are uncertain, as we did not evaluate the level of gene expression and isolate susceptibility to antibodies induced by vaccine antigens [28,40].

The potential impact of MenB vaccines on serogroup B meningococcal carriage remains unclear, with one U.K. evaluation suggesting that MenB-4C has little to no effect on reducing acquisition of meningococcal carriage [8]. Furthermore, recent evaluations at two U.S. universities suggest that vaccination with MenB-FHbp during serogroup B outbreaks does not rapidly reduce meningococcal carriage or reduce acquisition of meningococcal carriage following three vaccine doses [17,18]. Though we did not detect differences in carriage prevalence by MenACWY vaccination status, the recovery of few serogroup C or Y isolates and no serogroup W isolates among a highly-vaccinated university population suggests a potential impact of MenACWY on meningococcal carriage in U.S. university students. However, impact of MenACWY on meningococcal carriage in this population remains poorly understood, with a recent evaluation in the United Kingdom demonstrating a rise in serogroup W carriage despite 71% MenACWY vaccination coverage in university students [42].

In conclusion, results from our evaluation demonstrate that in the setting of high MenACWY vaccine coverage among a university population, the majority of meningococcal carriage is due to nongroupable strains, with low serogroup B carriage prevalence and a near absence of serogroups covered by the quadrivalent meningococcal conjugate vaccine. However, as serogroup B meningococcal disease outbreaks remain a public health concern at U.S. universities, these findings highlight the need to further evaluate serogroup B carriage and disease dynamics, in order to guide routine vaccination policy and outbreak response measures in this population.

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**Table 1**

Characteristics of participants by survey round at University A, March–April 2015.

Characteristic	One (N = 1076)		Two (N = 761)		Overall (N = 1837)	
	Total <sup>a</sup>	N (%)	Total <sup>a</sup>	N (%)	Total <sup>a</sup>	N (%)
Male sex	1073	432 (40.3)	761	371 (48.8)	1834	802 (43.7)
Median age in years (IQR)	1076	20 (19–21)	761	20 (19–21)	1837	20 (19–21)
Class year						
Freshman	1072	242 (22.6)	761	204 (26.8)	1833	446 (24.3)
Sophomore		267 (24.9)		167 (21.9)		433 (23.6)
Junior		229 (21.4)		172 (22.6)		401 (21.9)
Senior		334 (31.2)		218 (28.6)		552 (30.1)
Resides in residence hall	1076	830 (77.1)	761	592 (77.8)	1837	1422 (77.4)
Received MenACWY vaccine						
One dose	1076	662 (61.5)	761	447 (58.7)	1837	1109 (60.4)
Two doses		283 (26.3)		217 (28.5)		500 (27.2)
Frequent bars/parties 1 time per week	1076	591 (54.9)	761	412 (54.1)	1837	1003 (54.6)
Tobacco or marijuana use in past 30 days	1074	320 (29.8)	761	221 (29.0)	1835	541 (29.5)
Second-hand smoke exposure in past 30 days	1075	596 (55.4)	761	451 (59.3)	1836	1047 (57.0)
Antibiotic use in past 30 days	1074	109 (10.2)	761	77 (10.1)	1835	186 (10.1)
Upper respiratory tract infection in past 14 days	1072	536 (50.0)	761	201 (26.4)	1833	737 (40.2)

Abbreviations: MenACWY = quadrivalent meningococcal conjugate vaccine (serogroups A, C, W, Y), IQR = interquartile range.

<sup>a</sup>Total participants with known information.

**Table 2**

Prevalence of *N. meningitidis* carriage overall and by serogroup (slide agglutination) and capsular genotype (real-time polymerase chain reaction) among participants at University A, by survey round, March–April 2015.

Carriage	Round One (N = 1076)		Round Two (N = 761)	
	N	%	N	%
<i>N. meningitidis</i> carriage	137	12.7	111	14.6
<b>Slide agglutination</b>				
A	0	0	0	0
B	8	0.7	5	0.7
C	1	0.1	0	0
E	1	0.1	1	0.1
W	0	0	0	0
X	1	0.1	0	0
Y	1	0.1	0	0
Z	0	0	0	0
NG	125	11.6	105	13.8
<b>rt-PCR</b>				
A	0	0	0	0
B	19	1.8	20	2.6
C	2	0.2	2	0.3
W	0	0	0	0
X	2	0.02	2	0.3
Y	8	0.7	5	0.7
NG	106	9.9	82	10.8

Abbreviations: NG = Nongroupable, rt-PCR = real-time polymerase chain reaction.

Molecular typing profile of recovered isolates classified as capsular genotype B by real-time polymerase chain reaction among participants at University A, March–April 2015.

**Table 3**

Clonal complex (CC)	Sequence type	Number of isolates	PorA	FetA	FHbp	Oxford peptide ID		NhbA	NadA
							Subfamily/variant		
CC162	2153	1	P1.12-1,23-7	F1-12	865		A/v2-3	p0020	–
CC213	9413	1	P1.22,14	F5-5	45		A/v2-3	p0018	
CC23/Cluster A3	23	1	P1.5-2, 10-1	F4-1	25		A/v2-3	p0007	–
CC32/ET-5	11397	1	P1.18-1, 30-11	F3-3	510		B/v1	p0029	NadA-1.1
	11527	1	P1.22,14-6	F3-15	101		A/v2-3	p0237	–
	12750	1	P1.19,15	F3-3	21		A/v2-3	p0003	NadA-1.167
	33	3	P1.5,2	F5-1	144		B/v1	p0020	–
	32	1	P1.5,2-84	F3-3	21		A/v2-3	p0003	NadA-1.100
	10875	1	P1.5-2, 10-1	F5-1	144		B/v1	p0020	–
	11395	2	P1.7,16-111	F3-3	1		B/v1	p0003	NadA-1.1
CC35	35	2	P1.22-1,14	F1-34 <sup>a</sup>	16		A/v2-3	p0021	–
	11530	7	P1.22-1, 14	F1-76 <sup>a</sup>	16		A/v2-3	p0021	–
CC41/44 Lineage 3	11393	2	P1.22-25, 14-6	F1-5	499		A/v2-3	p0021	–
	136	2	P1.20, 23-3	F1-34	24		A/v2-3	p0010	–
	2578	1	P1.5-1,2-2	F1-5	100		B/v1	p0002	–
	7612	2	P1.18,25	F1-5	19		A/v2-3	p0002	–
	8052	1	P1.7-2,13-9	F1-5	14		B/v1	p0002	–
CC4821	3200	2	P1.17-6,23-6	F3-36	16		A/v2-3	p0669	–
CC750	2160	1	P1.22,1	F5-7	865		A/v2-3	p1018	–
	11394	1	P1.22,1	F5-7	16		A/v2-3	p1022	–
CC865	3327	1	P1.21,16-36	F5-8	119		A/v2-3	p0024	–
	865	1	P1.7-1,1	F1-6	19		A/v2-3	p0103	–
Unassigned	4221	3	P1.12-1,23-6	F1-151	13		B/v1	P0819	–
			P1.19-1,13-9	F5-148	106		A/v2-3	p0329	–
			P1.7-1,1	F5-148	4		B/v1	p0819	–

<sup>a</sup>Frame shift detected.

Table 4

Factors associated with *N. meningitidis* carriage among carriage survey participants at University A, March–April 2015.

Characteristic	Carrier (N = 248)		Non-carrier (N = 1589)		Bivariate analysis			Multivariable analysis		
	Total <sup>f</sup>	N (%)	Total <sup>f</sup>	N (%)	PR	95% CI	P-value	aPR	95% CI	P-value
Round										
One	248	137 (55.2)	1589	939 (59.1)	Ref	–	–	Ref	–	–
Two		111 (44.8)		650 (40.9)	1.18	1.03–1.37	0.02	<b>1.20</b>	<b>1.01–1.42</b>	<b>0.03</b>
Male sex <sup>a</sup>	246	151 (61.4)	1588	652 (41.1)	1.99	1.55–2.56	<0.01	<b>1.66</b>	<b>1.29–2.14</b>	<b>&lt;0.01</b>
Median age in years (IQR)	248	20 (19–21)	1589	20 (19–21)	1.00	0.98–1.03	0.75			
Class year										
Freshman	248	57 (23.0)	1585	389 (24.5)	Ref	–	–	–	–	–
Sophomore		67 (27.0)		367 (23.1)	1.19	0.84–1.70	0.32	–	–	–
Junior		50 (20.2)		351 (22.1)	1.01	0.69–1.47	0.97	–	–	–
Senior		74 (30.0)		478 (30.2)	1.07	0.76–1.52	0.69	–	–	–
Lives in residence hall <sup>b</sup>	248	180 (72.6)	1589	1242 (78.2)	0.76	0.58–0.99	0.04	0.85	0.66–1.10	0.23
Received MenACWY vaccine <sup>c</sup>										
One dose	248	161 (64.9)	1589	948 (59.7)	1.33	0.90–1.98	0.15	–	–	–
Two doses		64 (25.8)		436 (27.4)	1.23	0.80–1.89	0.35	–	–	–
Frequent bars/parties 1 time/week <sup>d</sup>	248	195 (78.6)	1589	808 (50.8)	2.62	1.99–3.45	<0.01	<b>2.03</b>	<b>1.52–2.72</b>	<b>&lt;0.01</b>
Tobacco or marijuana use in past 30 days <sup>e</sup>	248	125 (50.4)	1587	416 (26.2)	2.18	1.74–2.73	<0.01	<b>1.53</b>	<b>1.21–1.94</b>	<b>&lt;0.01</b>
Second-hand smoke exposure in past 30 days <sup>f</sup>	248	175 (70.6)	1588	872 (54.9)	1.67	1.33–2.10	<0.01	1.17	0.91–1.51	0.23
Used antibiotics in past 30 days <sup>g</sup>	242	11 (4.5)	1571	175 (11.1)	0.47	0.29–0.73	<0.01	<b>0.42</b>	<b>0.27–0.65</b>	<b>&lt;0.01</b>
Upper respiratory infection in past 14 days <sup>h</sup>	248	119 (48.0)	1585	618 (39.0)	1.27	1.05–1.53	0.01	<b>1.23</b>	<b>1.001–1.51</b>	<b>0.049</b>

Abbreviations: MenACWY = quadrivalent meningococcal conjugate vaccine (serogroups A, C, W, Y), IQR = interquartile range, PR = prevalence ratio.

Bold signifies significance at the  $P < 0.05$  level in the multivariable analysis.

Reference level:

<sup>a</sup>Female sex.

<sup>b</sup>Does not live in residence hall.



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- <sup>c</sup>Received no doses of MenACWY.
- <sup>d</sup>Frequents bars/parties < 1 time per week.
- <sup>e</sup>No tobacco or marijuana use in the past 30 days.
- <sup>f</sup>No second-hand smoke exposure in the past 30 days.
- <sup>g</sup>No antibiotics in the past 30 days.
- <sup>h</sup>No upper respiratory infection in the past 14 days.
- <sup>i</sup>Total participants with known information.